

FIG. 1

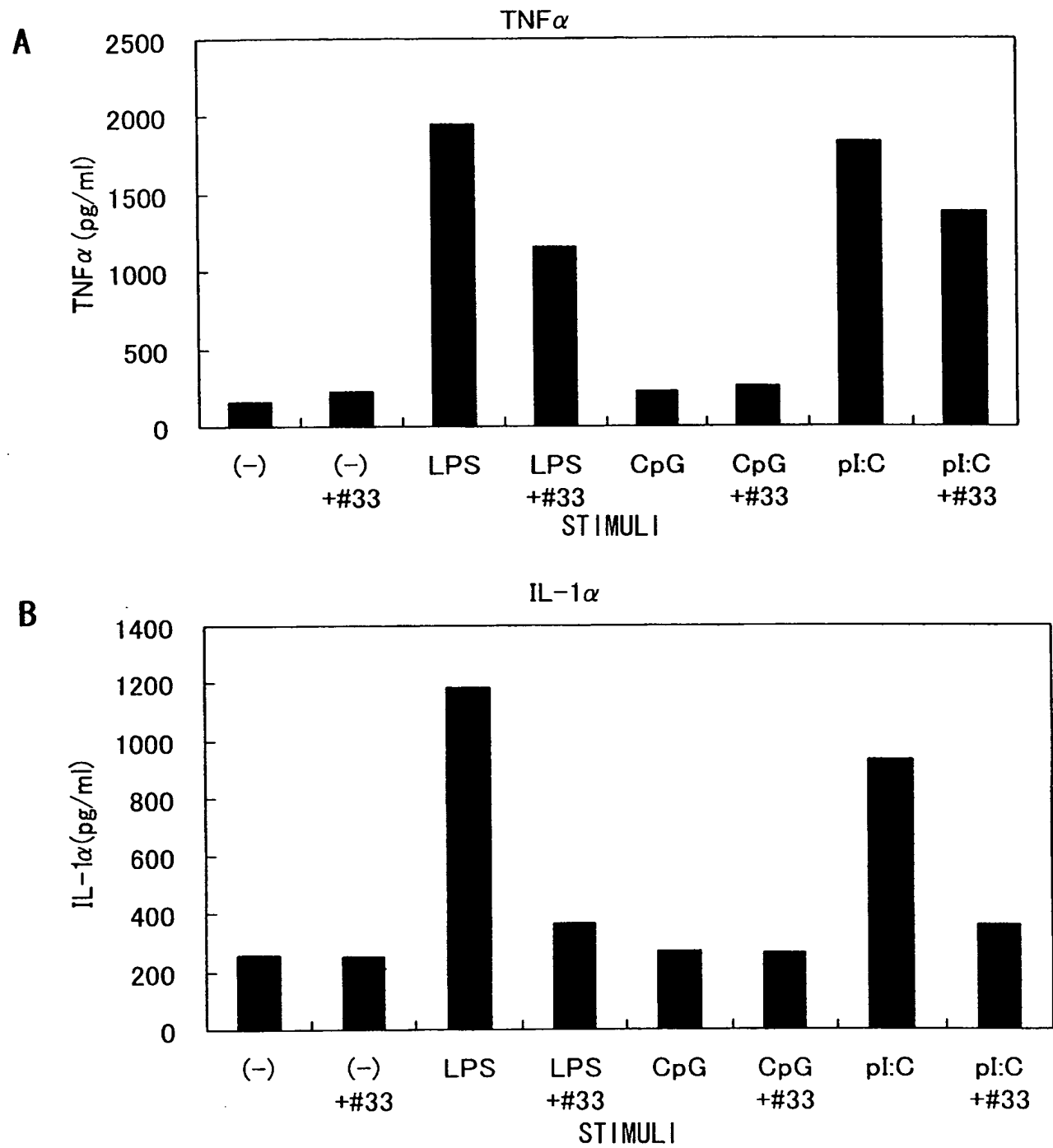


FIG. 2

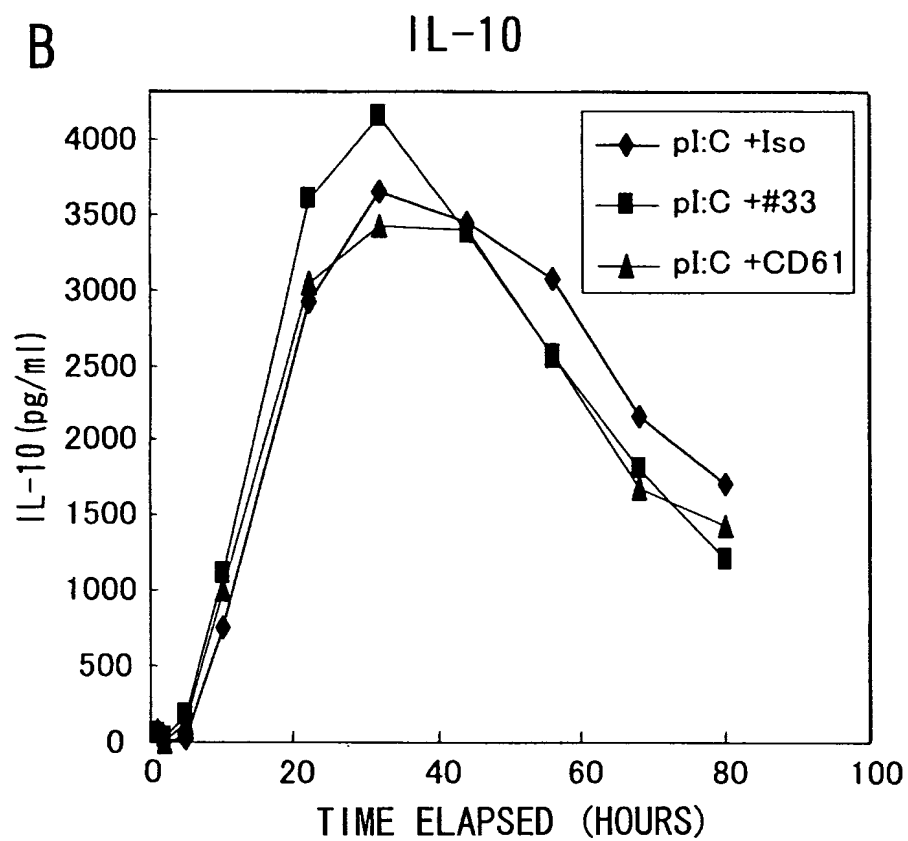
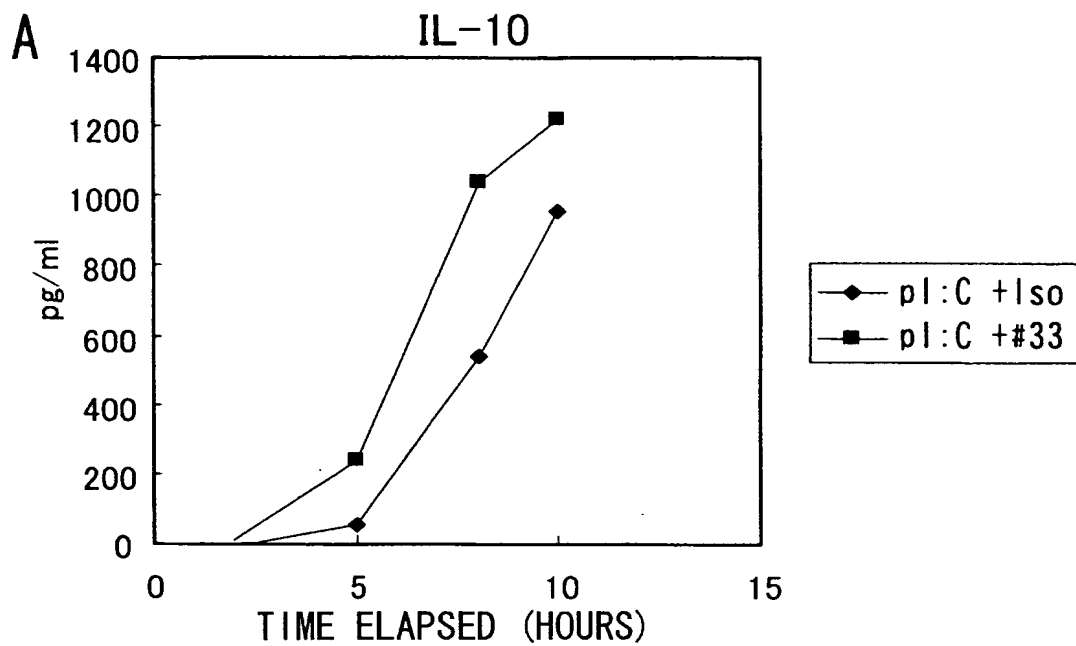


FIG. 3

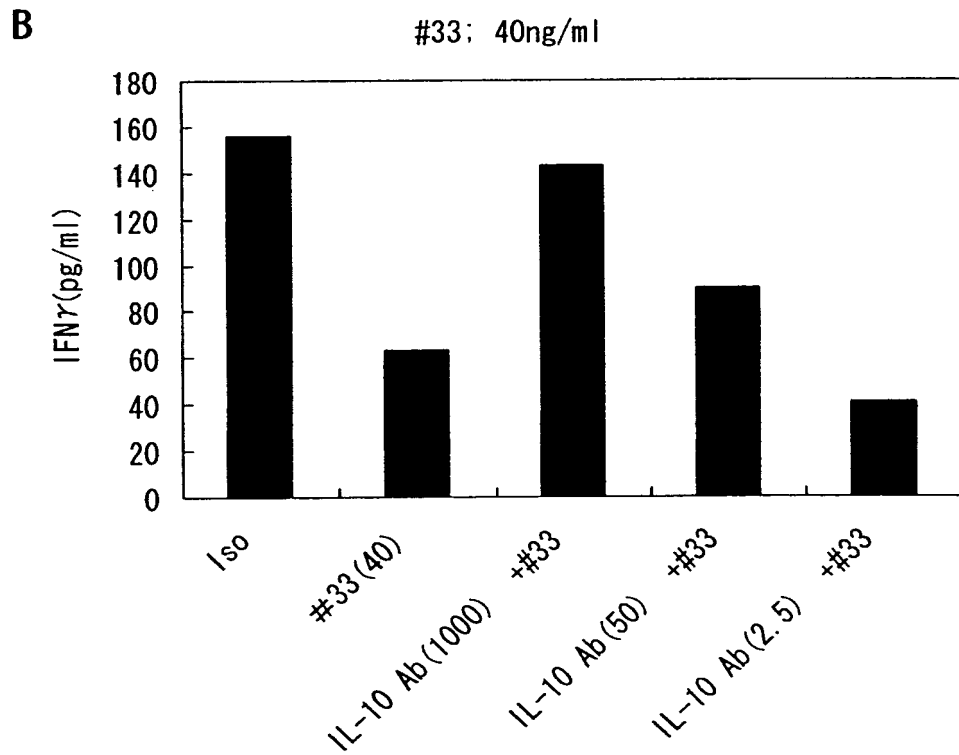
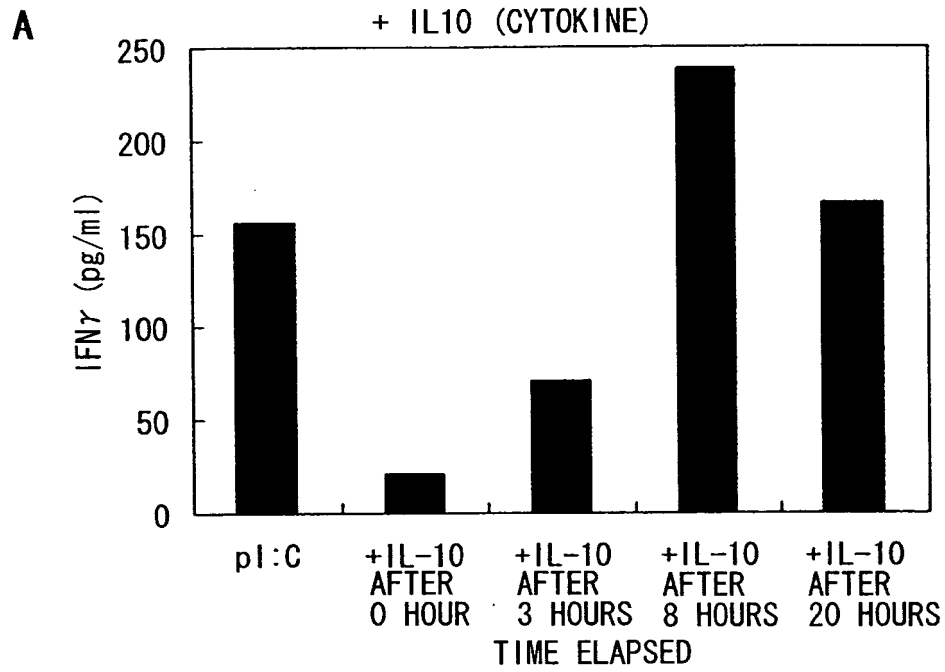


FIG. 4

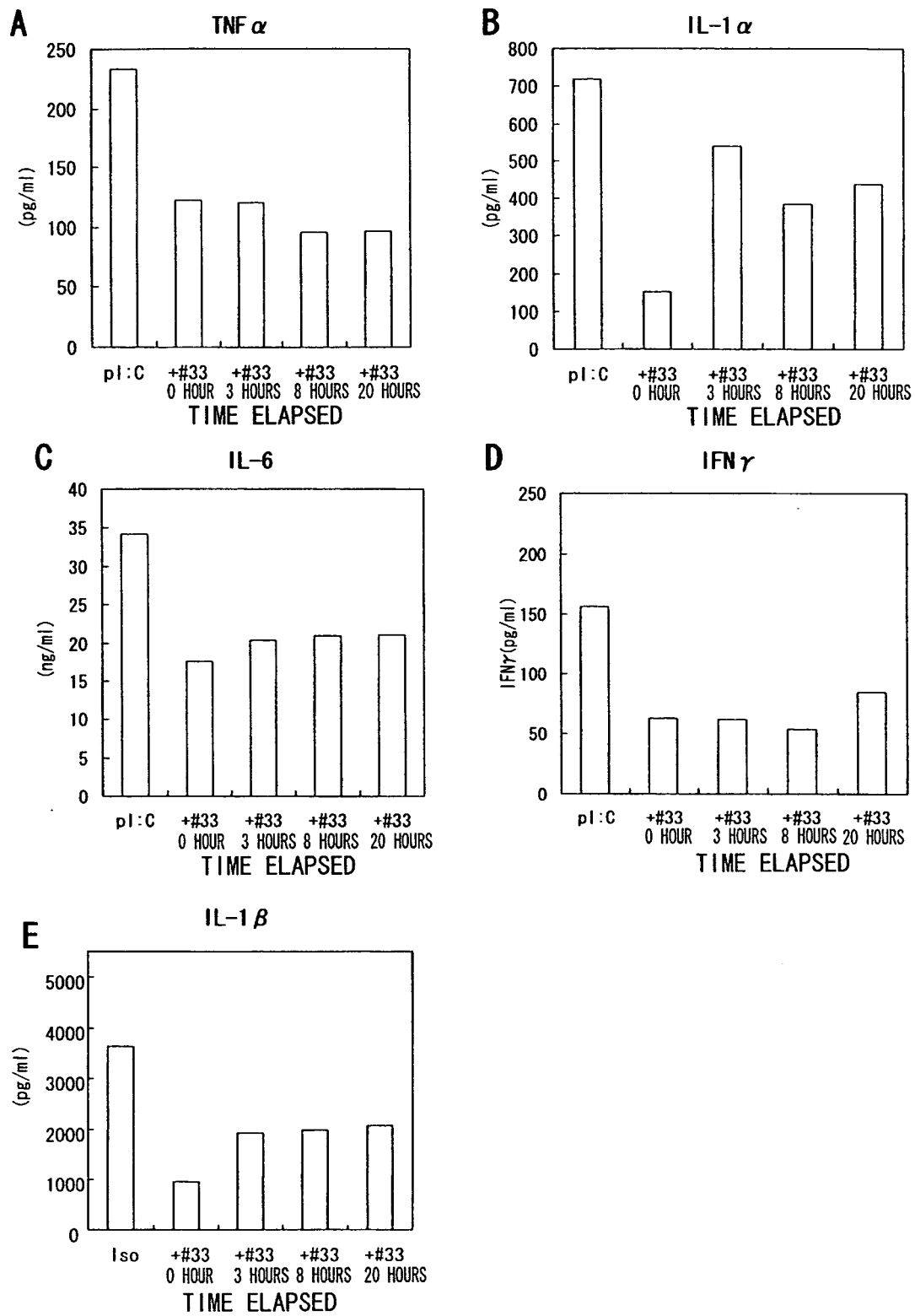


FIG. 5

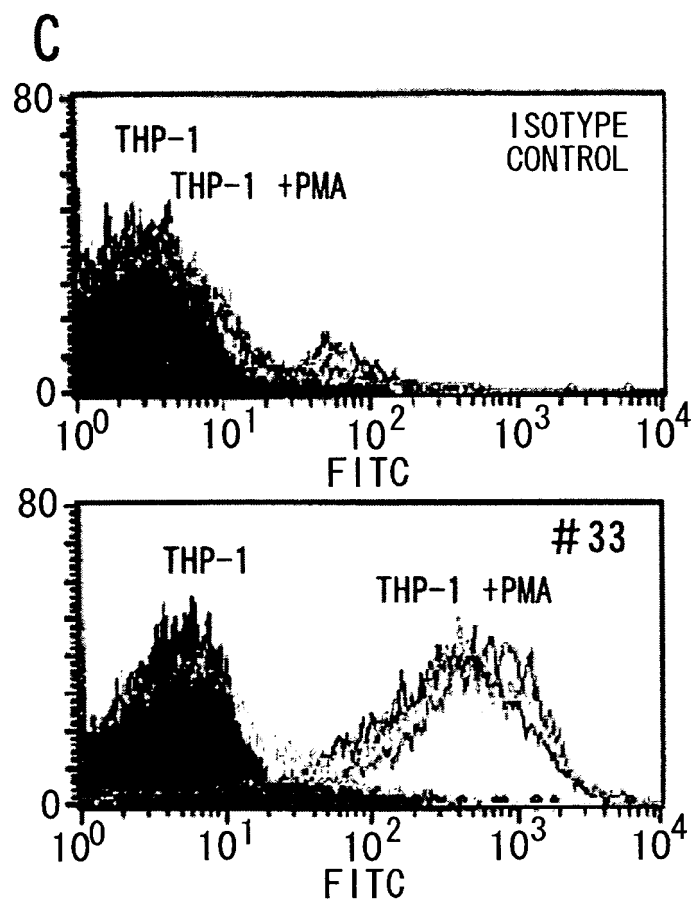
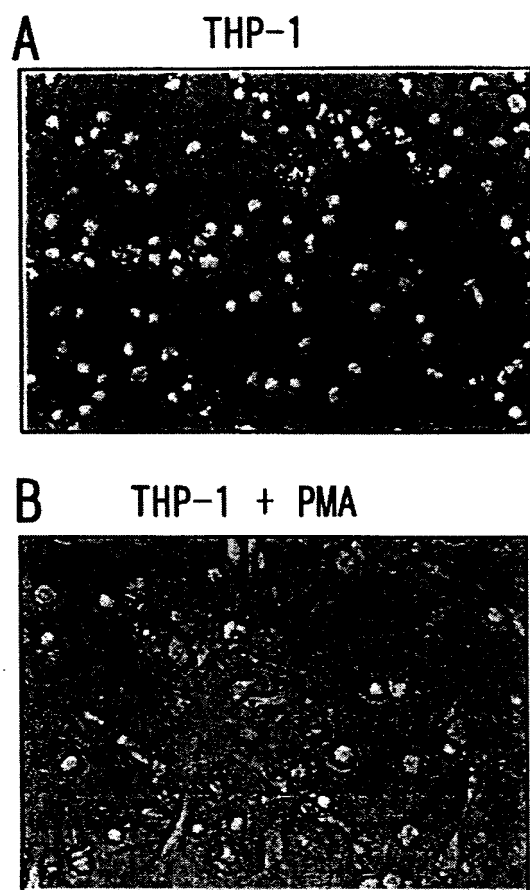


FIG. 6

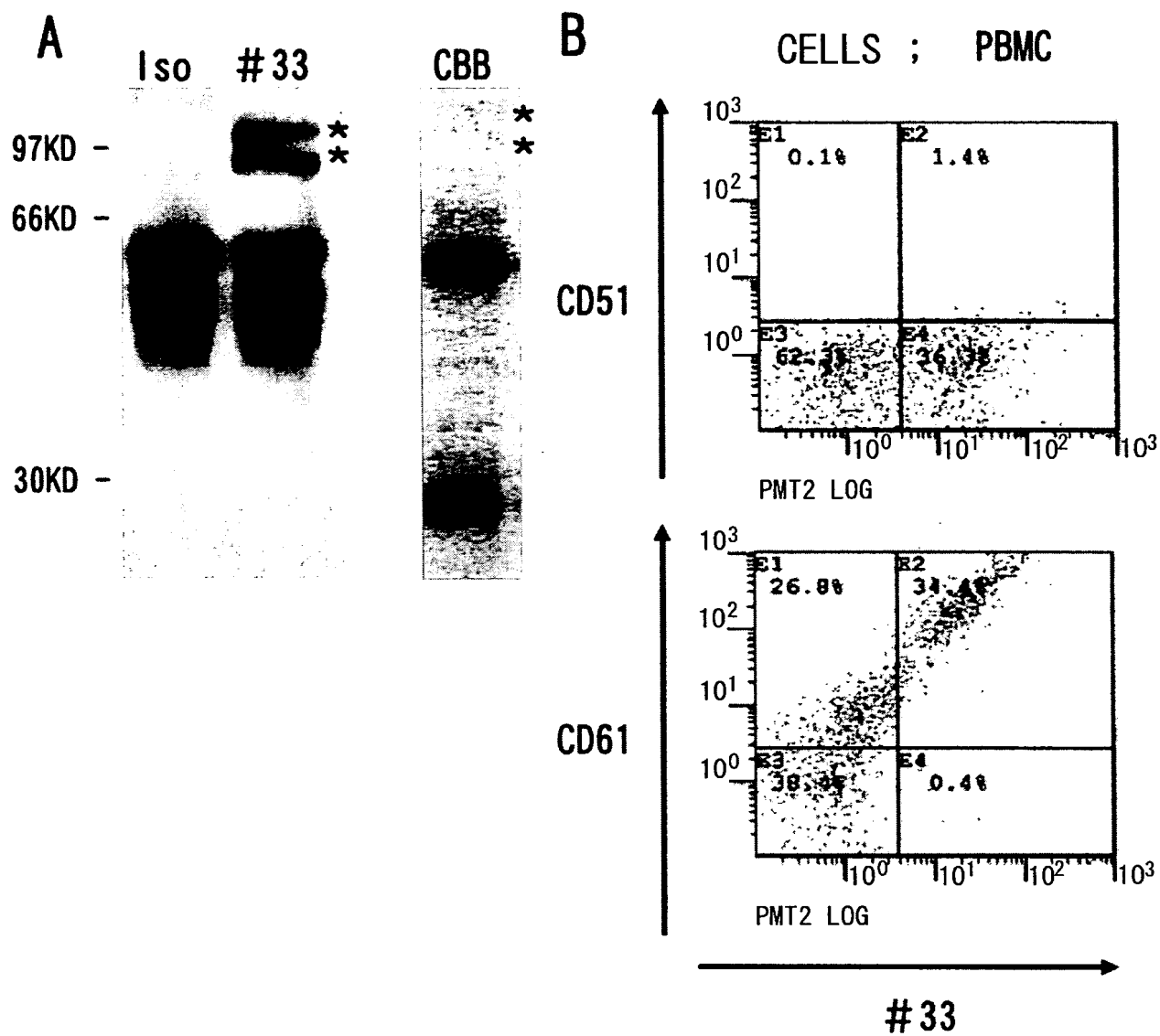


FIG. 7

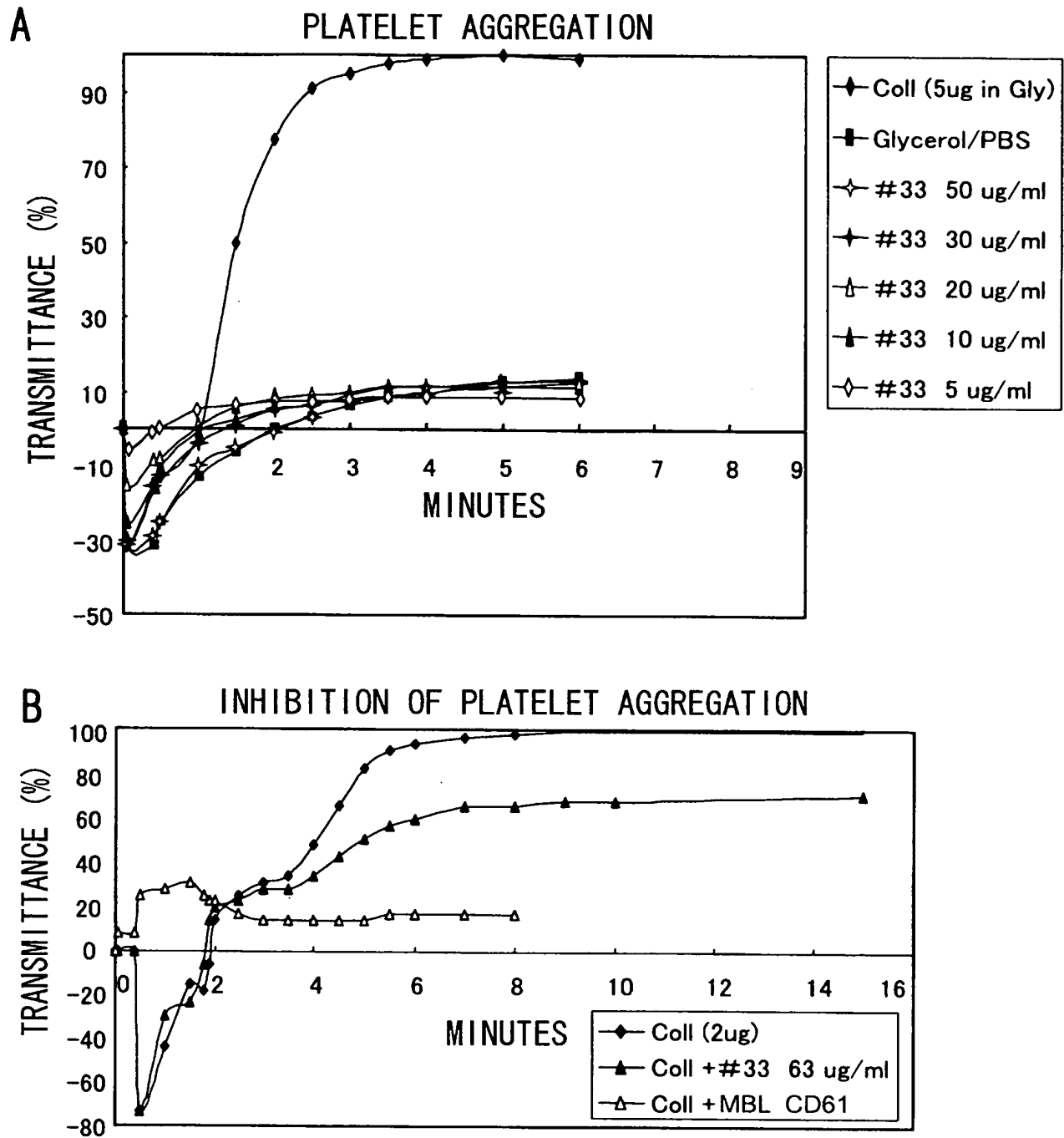


FIG. 8

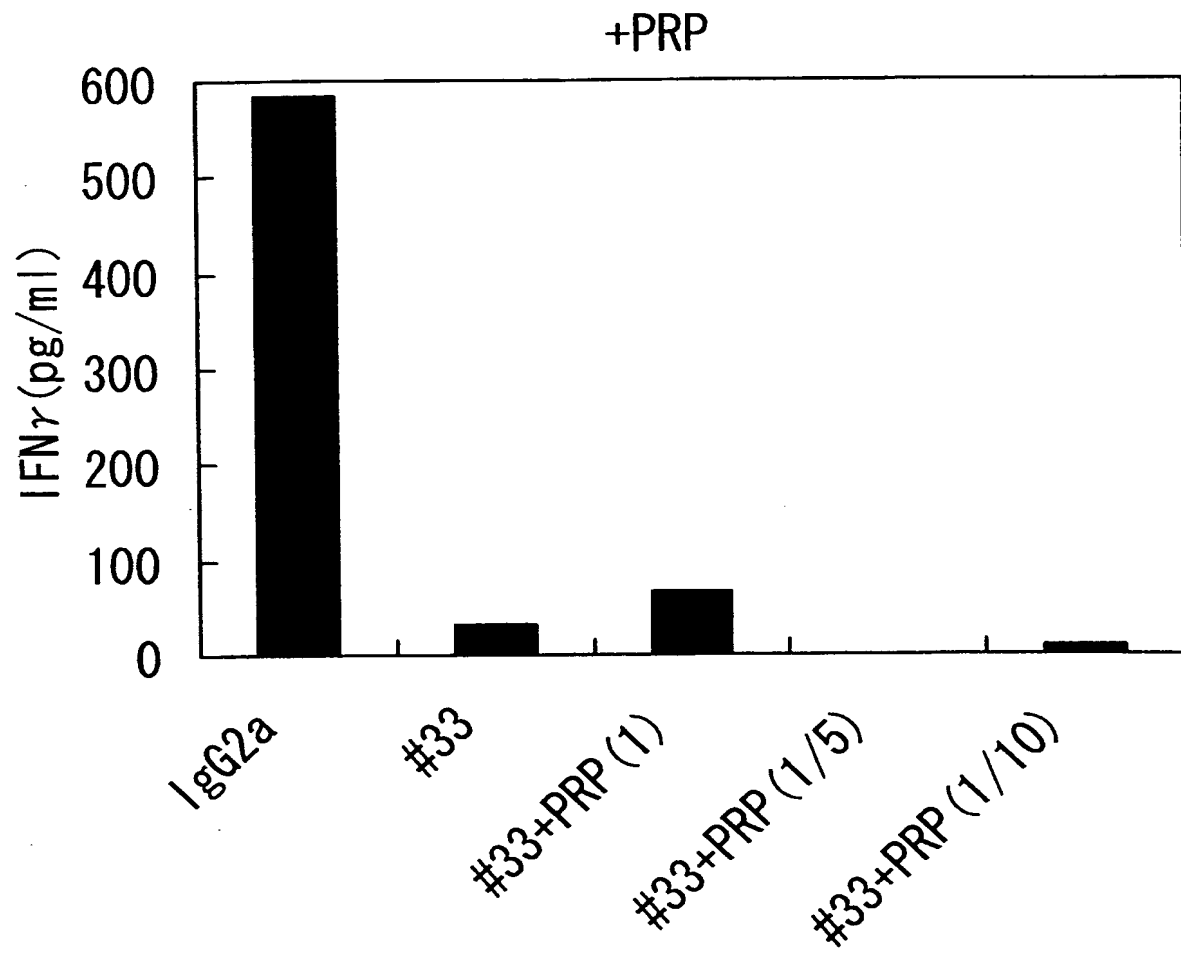


FIG. 9

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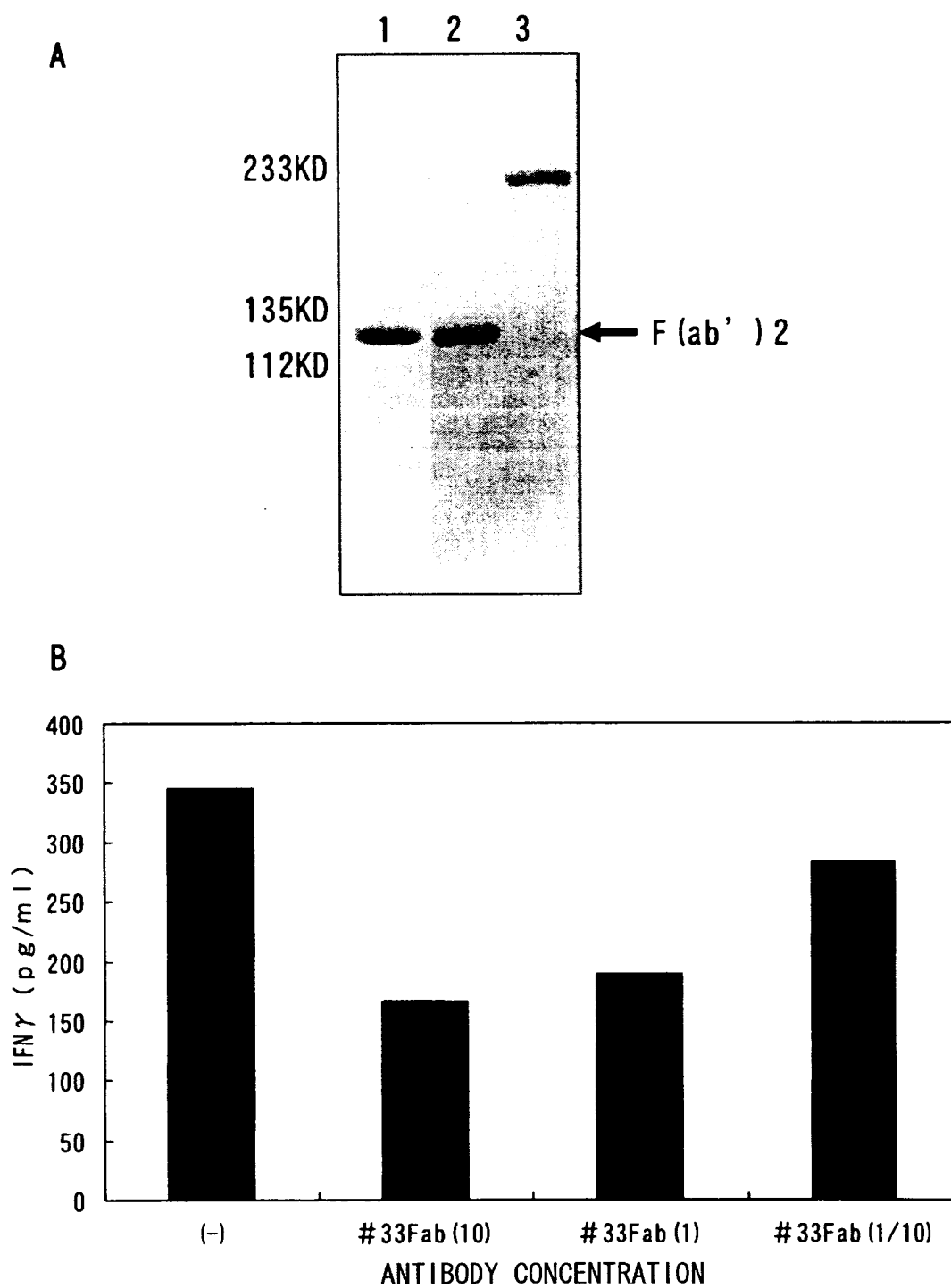


FIG. 10

#33 HEAVY CHAIN																			
10	20	30	40	50	60														
ATGGAATGGAGCGGGTCTTTATCTTCCTCCTGTCAGGAACTACAGGTGTCCACTCTGAG																			
M	E	W	S	G	V	F	I	F	L	L	S	G	T	T	G	V	H	S	E
70	80	90	100	110	120														
GTCCAGCTGCTACAGTCTGGACCTGAGCTGGTGAAGCCTGGAGCTTCAATGAAGATATCC																			
V	Q	L	L	Q	S	G	P	E	L	V	K	P	G	A	S	M	K	I	S
130	140	150	CDR1	160	170	180													
TGCAAGGCTTCTGGTTACTCATTCACTGGCTACACCATGAACTGGGTGAAGCAGAGCCAT																			
C	K	A	S	G	Y	S	F	T	G	Y	T	M	N	W	V	K	Q	S	H
190	200	210	CDR2	220	230	240													
GGAAAGAACCTTGAGTGGATTGGACTTATTAATCCTTACAGTGGTGTACTACCTACAAC																			
G	K	N	L	E	W	I	G	L	I	N	P	Y	S	G	V	T	T	Y	N
250	260	270	280	290	300														
CAGAGGTTCAAGGGCAAGGCCACATTAAGTGTAGACAAGTCATCCAGCACAGCCTACATG																			
Q	R	F	K	G	K	A	T	L	T	V	D	K	S	S	S	T	A	Y	M
310	320	330	340	350	360														
GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAACAACGGGGGGCT																			
E	L	L	S	L	T	S	E	D	S	A	V	Y	Y	C	A	T	R	G	A
370	CDR3	380	390	400	410	420													
CTGGGACAGGCGTACTACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA																			
L	G	Q	A	Y	Y	F	D	Y	W	G	Q	G	T	T	L	T	V	S	S
430	440	450																	
GCCAAAACAACAGCCCCATCGGTCTATCCACTG (SEQ ID NO: 12)																			
A K T T A P S V Y P L (SEQ ID NO: 4)																			

FIG. 11

#33 LIGHT CHAIN					
10	20	30	40	50	60
ATGGATT	TACAGGT	GCAGATT	TATCAGCT	TCCTGCT	AATCAGT
M	D	L	Q	V	Q
I	I	S	F	L	L
I	S	A	S	V	M
I	S				
70	80	90	100	110	120
AGAGG	ACAAATT	GTTCTC	ACCCAGT	CTCCAGT	TATCAT
R	G	Q	I	V	L
T	Q	S	P	V	I
M	S	A	S	P	G
E	R				
130	140	CDR1	150	160	170
GTCAC	CTTGAC	CTGCAG	TGCCAG	CTCAAG	TGTAA
V	T	L	T	C	S
A	S	S	S	V	N
Y	M	H	W	Y	Q
Q	K				
190	200	210	CDR2	220	230
TCAGG	CACCTC	CCCCAA	AAGATG	GATTTAT	GACACA
S	G	T	S	P	K
R	W	I	Y	D	T
S	K	L	A	S	G
V	P				
250	260	270	280	290	300
CCTCG	CTTCAG	TGGCAG	TGGGTT	cGGGAC	ATCATA
P	R	F	S	G	S
G	F	G	T	S	Y
S	L	T	I	T	N
M	E				
310	320	330	CDR3	340	350
GCTGA	AAGATG	CTGCCA	CTTATT	ACTGOC	CAGCAG
A	E	D	A	A	T
Y	Y	C	Q	Q	W
S	S	K	P	P	T
F	G				
370	380	390	400	410	420
TTTGG	GACCA	AAGCTG	GAGCTG	CAACGG	GCTGAT
F	G	T	K	L	E
L	Q	R	A	D	A
A	P	T	V	S	I
F	P				
430					
CCATCC	AGT	(SEQ	ID	NO: 16)	
P	S	S	(SEQ	ID	NO: 8)

FIG. 12